CLAIMS

1. A method of analysing microarray images, the method comprising the steps of:

receiving data from a microarray process,

modelling the microarray process to define a microarray model comprising at least one of target distribution defining a first independent sub-model and probe distribution defining a second independent sub-model,

comparing the received data with the microarray model in order to extract information from the data, and

outputting the information.

2. A method according to claim 1, wherein the data is received from a detector corresponding to a control target sample and a detector corresponding to a test target sample.

3. A method according to claim 2, wherein the model includes information about statistical similarity in the spot profile corresponding to each detector due to the spot profiles being formed from a common probe.

4. A method according to any preceding claim, wherein the microarray process is a DNA microarray process.

5. A method according to any preceding claim, wherein the extracted information is gene expression information.

6. A method according to any preceding claim, wherein when at least the second independent sub-model is employed in the modelling step, the second independent sub-model comprises a model of the spotting process.

7. A method according to claim 6, wherein the model of the spotting process includes an understanding of how adjacent spots interact.

8. A method according to any preceding claim, wherein the modelling step further comprises modelling the interaction between the background distribution of the received signal and at least one of target distribution and probe distribution.

9. A method according to claim 8, wherein the background distribution includes non-specific hybridication.

10. A method according to any preceding claim, wherein the modelling step further comprises modelling fluorescence to define a third independent sub-model.

11. A method according to claim 10, wherein the third independent sub-model includes information on the effect of DNA sequence on fluorescence.

12. A method according to any preceding claim, wherein the modelling step further comprises modelling hybridication to define a fourth independent sub-model.

13. A method according to claim 12, wherein the fourth independent sub-model includes information on the effect of sequence on hybridication.

14. A method according to any preceding claim, wherein the modelling step further comprises modelling spatial variation of target concentration.

15. A method according to any preceding claim, wherein the comparing step further comprises comparing the received image data with the microarray model in order to predict missing data.

16. A method according to claim 15, wherein the missing data is due to saturation in the device which creates the image data.

17. A method according to any preceding claim, wherein the modelling step further comprises modelling detector nonlinearity.

18. A method according to any preceding claim, wherein the structure of the microarray model is hierarchical.

19. A method according to any preceding claim, wherein the data received from the microarray process is image data.

20. A method according to any of claims 1 to 18, wherein the data received from the microarray process is pre-analysed data.

21. A method according to any preceding claim, wherein standard Markov chain Monte Carlo methods are employed.

22. An apparatus for analysing microarray images, the apparatus comprising:

means for receiving data from a microarray process,

means for modelling the microarray process to define a microarray model comprising at least one of target distribution defining a first independent sub-model and probe distribution defining a second independent sub-model,

means for comparing the received data with the microarray model in order to extract information from the data, and

means for outputting the information.

23. An apparatus according to claim 22, wherein the data is received from a channel corresponding to a control target sample and a channel corresponding to a test target sample.

24. An apparatus according to claim 22 or claim 23, wherein the microarray process is a DNA microarray process.

25. An apparatus according to any of claims 22 to 24, wherein the extracted information is gene expression information.

26. An apparatus according to any of claims 22 to 25, wherein the means for modelling further comprises means for modelling the interaction between the background distribution of the received signal and at least one of target distribution and probe distribution.

27. An apparatus according to any claims 22 to 26, wherein the means for modelling further comprises means for modelling fluorescence to define a third independent sub-model.

28. An apparatus according to any of claims 22 to 27, wherein the means for modelling further comprises means for modelling hybridication to define a fourth independent sub-model.

29. An apparatus according to any of claims 22 to 28, wherein the means for modelling further comprises means for modelling spatial variation of target concentration.

30. An apparatus according to any claims 22 to 29, wherein the means for comparing further comprises means for comparing the received image data with the microarray model in order to predict missing data.

31. An apparatus according to any of claims 22 to 30, wherein the means for modelling further comprises means for modelling detector nonlinearity.

32. An apparatus according to any of claims 22 to 31 wherein the data received from the microarray process is image data.

33. An apparatus according to any of claims 22 to 31, wherein the data received from the microarray process is pre-analysed data.